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Timestamp: [year=2008; month=8; day=11; hr=17; min=28; sec=25; ms=669;]

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Application No: 10591752 Version No: 2.0

Input Set:

Output Set:

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Finished: 2008-07-09 14:53:34.029
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Total Warnings: 11
Total Errors: 0
No. of SeqIDs Defined: 18
Actual SeqID Count: 18

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W 213	Artificial or Unknown found in <213> in SEQ ID (10)
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SEQUENCE LISTING

<110> YOKOTA, Akiho
 SHIGEOKA, Shigeru
 TOMIZAWA, Ken-ichi

<120> METHOD FOR IMPROVING PRODUCTIVITY OF PLANT BY CHLOROPLAST
 TECHNOLOGY

<130> 2006_1303A

<140> 10591752
 <141> 2008-07-09

<150> PCT/JP2005/004037
 <151> 2005-03-02

<150> JP 2004-059513
 <151> 2004-03-03

<160> 18

<170> PatentIn version 3.4

<210> 1
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 <212> PRT
 <213> Spinacia oleracea L

<220>

<223> Fructose-1,6-bisphosphatase

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Lys Tyr Glu Ile Glu Thr Leu Thr Gly Trp Leu Leu Lys Gln Glu Met
 20 25 30

Ala Gly Val Ile Asp Ala Glu Leu Thr Ile Val Leu Ser Ser Ile Ser
 35 40 45

Leu Ala Cys Lys Gln Ile Ala Ser Leu Val Gln Arg Ala Gly Ile Ser
 50 55 60

Asn Leu Thr Gly Ile Gln Gly Ala Val Asn Ile Gln Gly Glu Asp Gln
 65 70 75 80

Lys Lys Leu Asp Val Val Ser Asn Glu Val Phe Ser Ser Cys Leu Arg
85 90 95

Ser Ser Gly Arg Thr Gly Ile Ile Ala Ser Glu Glu Glu Asp Val Pro
100 105 110

Val Ala Val Glu Glu Ser Tyr Ser Gly Asn Tyr Ile Val Val Phe Asp
115 120 125

Pro Leu Asp Gly Ser Ser Asn Ile Asp Ala Ala Val Ser Thr Gly Ser
130 135 140

Ile Phe Gly Ile Tyr Ser Pro Asn Asp Glu Cys Ile Val Asp Ser Asp
145 150 155 160

His Asp Asp Glu Ser Gln Leu Ser Ala Glu Glu Gln Arg Cys Val Val
165 170 175

Asn Val Cys Gln Pro Gly Asp Asn Leu Leu Ala Ala Gly Tyr Cys Met
180 185 190

Tyr Ser Ser Ser Val Ile Phe Val Leu Thr Ile Gly Lys Gly Val Tyr
195 200 205

Ala Phe Thr Leu Asp Pro Met Tyr Gly Glu Phe Val Leu Thr Ser Glu
210 215 220

Lys Ile Gln Ile Pro Lys Ala Gly Lys Ile Tyr Ser Phe Asn Glu Gly
225 230 235 240

Asn Tyr Lys Met Trp Asp Asp Lys Leu Lys Lys Tyr Met Asp Asp Leu
245 250 255

Lys Glu Pro Gly Glu Ser Gln Lys Pro Tyr Ser Ser Arg Tyr Ile Gly
260 265 270

Ser Leu Val Gly Asp Phe His Arg Thr Leu Leu Tyr Gly Gly Ile Tyr
275 280 285

Gly Tyr Pro Arg Asp Ala Lys Ser Lys Asn Gly Lys Leu Arg Leu Leu
290 300

Tyr Glu Cys Ala Pro Met Ser Phe Ile Val Glu Gln Ala Gly Gly Lys

305 310 315 320

Gly Ser Asp Gly His Gln Arg Ile Leu Asp Ile Gln Pro Thr Glu Ile
325 330 335

His Gln Arg Val Pro Leu Tyr Ile Gly Ser Val Glu Glu Val Glu Lys
340 345 350

Leu Glu Lys Tyr Leu Ala
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<210> 2
<211> 1074
<212> DNA
<213> Spinacia oleracea L

<220>

<223> Fructose-1,6-bisphosphatase

<400> 2
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accatcggtc tttctagcat ttcattggct tgtaaacaaa ttgcttcctt ggttcaacga 180
gctgggtatct ctaacttgac tggaattcaa ggtgctgtca atatccaagg agaggatcag 240
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ttgaggcttt tgtatgaatg tgcacctatg agttttattg ttgaacaagc tgggtgtaaa 960

ggttctgatg gtcacaaaag aattcttgac attcaacca ccgagatata tcaacgtgtg 1020

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<211> 333

<212> PRT

<213> Spinacia oleracea L

<220>

<223> Sedoheptulose-1, 7-bisphosphatase

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Val Asn Lys Ala Lys Asn Ser Ser Leu Val Thr Lys Cys Glu Leu Gly
1 5 10 15

Asp Ser Leu Glu Glu Phe Leu Ala Lys Ala Thr Thr Asp Lys Gly Leu
20 25 30

Ile Arg Leu Met Met Cys Met Gly Glu Ala Leu Arg Thr Ile Gly Phe
35 40 45

Lys Val Arg Thr Ala Ser Cys Gly Gly Thr Gln Cys Val Asn Thr Phe
50 55 60

Gly Asp Glu Gln Leu Ala Ile Asp Val Leu Ala Asp Lys Leu Leu Phe
65 70 75 80

Glu Ala Leu Asn Tyr Ser His Phe Cys Lys Tyr Ala Cys Ser Glu Glu
85 90 95

Leu Pro Glu Leu Gln Asp Met Gly Gly Pro Val Asp Gly Gly Phe Ser
100 105 110

Val Ala Phe Asp Pro Leu Asp Gly Ser Ser Ile Val Asp Thr Asn Phe
115 120 125

Ser Val Gly Thr Ile Phe Gly Val Trp Pro Gly Asp Lys Leu Thr Gly
130 135 140

Val Thr Gly Arg Asp Gln Val Ala Ala Ala Met Gly Ile Tyr Gly Pro
145 150 155 160

Arg Thr Thr Tyr Val Leu Ala Leu Lys Asp Tyr Pro Gly Thr His Glu
165 170 175

Phe Leu Leu Leu Asp Glu Gly Lys Trp Gln His Val Lys Glu Thr Thr
180 185 190

Glu Ile Asn Glu Gly Lys Leu Phe Cys Pro Gly Asn Leu Arg Ala Thr
195 200 205

Ser Asp Asn Ala Asp Tyr Ala Lys Leu Ile Gln Tyr Tyr Ile Lys Glu
210 215 220

Lys Tyr Thr Leu Arg Tyr Thr Gly Gly Met Val Pro Asp Val Asn Gln
225 230 235 240

Ile Ile Val Lys Glu Lys Gly Ile Phe Thr Asn Val Ile Ser Pro Thr
245 250 255

Ala Lys Ala Lys Leu Arg Leu Leu Phe Glu Val Ala Pro Leu Gly Phe
260 265 270

Leu Ile Glu Lys Ala Gly Gly His Ser Ser Glu Gly Thr Lys Ser Val
275 280 285

Leu Asp Ile Glu Val Lys Asn Leu Asp Asp Arg Thr Gln Val Ala Tyr
290 295 300

Gly Ser Leu Asn Glu Ile Ile Arg Phe Glu Lys Thr Leu Tyr Gly Ser
305 310 315 320

Ser Arg Leu Glu Glu Pro Val Pro Val Gly Ala Ala Ala
325 330

<210> 4
<211> 999
<212> DNA
<213> Spinacia oleracea L

<220>

<223> Sedoheptulose-1,7-bisphosphatase

<400> 4

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gaagcattaa ggaccattgg ctttaaagtg aggactgctt catgtggtgg aactcaatgt 180
gttaacacct ttggagacga acagcttgcc attgatgtgc ttgctgacaa gcttcttttc 240
gaggcattga actattcaca cttctgcaag tatgcttggt cagaagaact ccttgagctt 300
caagatatgg gagggcccgt tgatggcgga ttcagtgtag catttgaccc ccttgatgga 360
tccagcattg tcgataccaa tttctcagtt gggaccatat tcggggtttg gccaggtgac 420
aagctaactg gtgtaacagg cagagatcaa gtggctgctg caatgggaat ttatggctct 480
aggactactt atgttctcgc tcttaaggac taccctggca cccatgaatt tcttcttctt 540
gatgaaggaa agtggcaaca tgtgaaagaa acaacagaaa tcaatgaagg aaaattgttc 600
tgtcctggaa acttgagagc cacttctgac aatgctgatt atgctaagct gattcaatac 660
tatataaaag agaaatacac attgagatac actggaggaa tggttcctga tgttaaccag 720
atcatagtga aggagaaagg tatattcaca aatgtaatat cacctacagc caaggcaaag 780
ttgaggttac tgtttgaggt agctcctcta gggttcttga ttgagaaggc tgggtggcac 840
agcagtgagg gaaccaagtc tgtgttgac attgaagtca aaaaccttga tgacagaacc 900
caagttgctt acggctcctt gaacgagatc atccgatttg agaagacact atacggatcc 960
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<210> 5

<211> 356

<212> PRT

<213> Synechococcus

<220>

<223> fructose-1,6-bisphosphatase/sedoheptulose-1,7-bisphosphatase from
Synechococcus PCC 7942

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Met Glu Lys Thr Ile Gly Leu Glu Ile Ile Glu Val Val Glu Gln Ala
1 5 10 15

Ala Ile Ala Ser Ala Arg Leu Met Gly Lys Gly Glu Lys Asn Glu Ala
20 25 30

Asp Arg Val Ala Val Glu Ala Met Arg Val Arg Met Asn Gln Val Glu
35 40 45

Met Leu Gly Arg Ile Val Ile Gly Glu Gly Glu Arg Asp Glu Ala Pro
50 55 60

Met Leu Tyr Ile Gly Glu Glu Val Gly Ile Tyr Arg Asp Ala Asp Lys
65 70 75 80

Arg Ala Gly Val Pro Ala Gly Lys Leu Val Glu Ile Asp Ile Ala Val
85 90 95

Asp Pro Cys Glu Gly Thr Asn Leu Cys Ala Tyr Gly Gln Pro Gly Ser
100 105 110

Met Ala Val Leu Ala Ile Ser Glu Lys Gly Gly Leu Phe Ala Ala Pro
115 120 125

Asp Phe Tyr Met Lys Lys Leu Ala Ala Pro Pro Ala Ala Lys Gly Lys
130 135 140

Glu Thr Ser Ile Lys Ser Ala Thr Glu Asn Leu Lys Ile Leu Ser Glu
145 150 155 160

Cys Leu Asp Arg Ala Ile Asp Glu Leu Val Val Val Val Met Asp Arg
165 170 175

Pro Arg His Lys Glu Leu Ile Gln Glu Ile Arg Gln Ala Gly Ala Arg
180 185 190

Val Arg Leu Ile Ser Asp Gly Asp Val Ser Ala Ala Ile Ser Cys Gly
195 200 205

Phe Ala Gly Thr Asn Thr His Ala Leu Met Gly Ile Gly Ala Ala Pro
210 215 220

Glu Gly Val Ile Ser Ala Ala Ala Met Arg Cys Leu Gly Gly His Phe
225 230 235 240

Gln Gly Gln Leu Ile Tyr Asp Pro Glu Val Val Lys Thr Gly Leu Ile
245 250 255

Gly Glu Ser Arg Glu Ser Asn Ile Ala Arg Leu Gln Glu Met Gly Ile
260 265 270

Thr Asp Pro Asp Arg Val Tyr Asp Ala Asn Glu Leu Ala Ser Gly Gln
 275 280 285

Glu Val Leu Phe Ala Ala Cys Gly Ile Thr Pro Gly Leu Leu Met Glu
 290 295 300

Gly Val Arg Phe Phe Lys Gly Gly Ala Arg Thr Gln Ser Leu Val Ile
 305 310 315 320

Ser Ser Gln Ser Arg Thr Ala Arg Phe Val Asp Thr Val His Met Phe
 325 330 335

Asp Asp Val Lys Thr Val Ser Leu Pro Leu Ile Pro Asp Pro Lys Trp
 340 345 350

Arg Pro Glu Arg
 355

<210> 6
 <211> 1312
 <212> DNA
 <213> Synechococcus

<220>

<223> fructose-1,6-bisphosphatase/sedoheptulose-1,7-bisphosphatase from
 Synechococcus PCC 7942

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 gaatccccag aagcaatcat ccgtaaggag tcaggacggc gtggagaaga cgatcggtct 120
 cgagattatt gaagttgtcg agcaggcagc gatcgctctg gcccgctga tgggcaaagg 180
 cgaaaagaat gaagccgatc gcgtcgagc agaagcgatg cgggtgcgga tgaaccaagt 240
 ggaaatgctg ggccgcatcg tcatcggtga aggcgagcgc gacgaagcac cgatgctcta 300
 tatcggtgaa gaagtgggca tctaccgca tgcagacaag cgggctggcg taccggtgg 360
 caagctggtg gaaatcgaca tcgccgttga cccctgcgaa ggcaccaacc tctgcgccta 420
 cggtcagccc ggctcgatgg cagttttggc catctccgag aaaggcggcc tgtttgcagc 480
 tcccgaactt tacatgaaga aactggctgc acccccagct gccaaaggca aagagacatc 540
 aataaagtcc gcgaccgaaa acctgaaaat tctctcgga tgtctcgatc gcgccatcga 600

tgaattggtg gtcgtggtca tggatcgtec ccgccacaaa gagctaatacc aagagatccg	660
ccaagcgggt gccgcgtcc gtctgatcag cgatggtgac gtttcggccg cgatctcctg	720
cggttttgct ggcaccaaca cccacgcctt gatgggcata ggtgcagctc ccgagggtgt	780
gatttcggca gcagcaatgc gttgectcgg cgggcacttc caaggccagc tgatctacga	840
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gcaagaaatg ggcatacccg atcccgatcg tgtctacgac gcgaacgaac tggcttcggg	960
tcaagaagtg ctgtttgcgg cttgcggtat caccgccggc ttgctgatgg aaggcgtgcg	1020
cttcttcaaa ggccggcgctc gcacccagag cttggtgatc tccagccagt cacggacggc	1080
tcgcttcgtt gacaccgttc acatgttcga cgatgtcaaa acggttagcc tgccgttaat	1140
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tgtttttcag cgaatccatt tgcgatcgct tttcaaacc ttttttcgtc aaccttcttt	1260
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<210> 7
 <211> 133
 <212> DNA
 <213> Nicotiana tabacum

<220>

<223> psbA promoter

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aagccttcca ttttctatit tgatttgtag aaaactagtg tgcttgggag tcctgatga	120
ttaaataaac caa	133

<210> 8
 <211> 159
 <212> DNA
 <213> Nicotiana tabacum

<220>

<223> rps16 terminator

<400> 8	
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tatataactt tgtatgactt ttctcttcta tttttttgta tttcctccct ttccttttct	120

atttgtatTT ttttatcatt gcttccattg aattactag

159

<210> 9

<211> 805

<212> DNA

<213> Escherichia coli

<220>

<223> aadA

<400> 9

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gcgtcatcga gcgccatctc gaaccgacgt tGctggccgt acatttgtac ggctccgcag 120

tggatggcgg cctgaagcca cacagtGata ttgatttgct ggttacggTg accgtaaggc 180

ttgatgaaac aacgcggcga gctttgatca acgacctttt ggaaacttcg gcttccctg 240

gagagagcga gattctccgc gctgtagaag tcaccattgt tgtgcacgac gacatcatTc 300

cgtggcgTta tccagctaag cgcgaactgc aatttggaga atggcagcgc aatgacatTc 360

ttgcaggtat cttcgagcca gccacgatcg acattgatct ggctatctTg ctgacaaaag 420

caagagaaca tagcgTtgcc ttggtaggTc cagcggcgga ggaactcttt gatccggtTc 480

ctgaacagga tctattTgag gcgctaaatg aaaccttaac gctatggaac tcgccgcccG 540

actgggctgg cGatgagcga aatgtagTgc ttacgtTgTc ccgcattTgg tacagcgcag 600

taaccggcaa aatcgcgccg aaggatgTcg ctgccgactg ggcaatggag cgctgcccG 660

cccagtatca gcccgTcata cttgaagcta gacaggctta tcttggacaa gaagaagatc 720

gcttggcctc gcgcgcagat cagttggaag aatttgtcca ctacgtgaaa ggcgagatca 780

ctaaggtagt tggcaaataa ctgca 805

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<213> Artificial sequence

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<223> synthetic construct

<220>

<223> pLD6

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ggaagagtat gagtattcaa catttcctg tcgcccttat tccctTTTTt gcggcatttt	180
gccttcctgt ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt	240
tgggtgcacg agtgggttac atcgaactgg atctcaacag cggtaaagatc cttgagagtt	300
ttcgccccga agaacgtttt ccaatgatga gcactTTTaa agttctgcta tgtggcgcgg	360
tattatcccg tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga	420
atgacttggg tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa	480
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